

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Fowler, Timothy  
Stuart, Causey
- (ii) TITLE OF THE INVENTION: ENTEROBACTERIACEAE FERMENTATION STAINS
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genencor International, Inc.
  - (B) STREET: 925 Page Mill Road
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: US
  - (F) ZIP: 94304-1013
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/876,132
  - (B) FILING DATE: 23-JUN-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Glaister, Debra J.
  - (B) REGISTRATION NUMBER: 33,888
  - (C) REFERENCE/DOCKET NUMBER: GC372
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-846-7620
  - (B) TELEFAX: 650-845-6504

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1660 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGATCTACAC AAGGCAAATT GAAAAAATAG ATAAATTTT CGCAGGTATT AAAGCCGACT	60
TAAACAAAT GAGTGAAGAA GAAAGAAAA AAATAAATAC ATATTTTGAG TTAGTAAAAG	120
AGAAAGAAAA AATAAAGAA GACCTCGGCT TAACAGTCGA AAAACCAGAA ATAATAAAAA	180
GAAAGAGACT GTGATTTTTA ATGGAAATCG TGAGGAAAAG AAAATTTTAA TTTTCATTTT	240
CGAGGGATTA ATTTGTTGTA AGTTGATGAA AAATCTAGAT AAAAAATGCA GATCAAAAAT	300

GTGTTGAATT	TGACATTATT	GAAATACGTA	GTATATCAAT	AATGGGGGTT	TGTCTATTTT	360
ATTTTGCAG	GATTGAAAAT	CTGAGTGAAA	GAAAATAGTT	TGCGAGAGCA	AAAAAACCTT	420
TGCCGTTTTT	TTCAAATGAC	TTTGGAAAAA	ATTCATTGTG	AGCGGTAGCG	AAACTTTGAA	480
ATTTTTTACA	TTGGAAATTT	GAAAAAATAA	GGCAAAAGAA	ACTCAAATGG	AAAAATATT	540
ATTATAAAAA	AAGGAGATCG	GATATGGATT	TTAAAAGCAG	AAAACGACA	TTGAATGAAA	600
AAAAAGATTT	GGAAAAATC	TATGCTGAGA	GTGAATTTAA	AGCAAAAAAA	TTGGGAACCT	660
AACCCGGTGT	TGTTTTAGAA	ATGACGATGA	AAGAAATGAT	GAAAAATATC	AACCTCGATG	720
TTAATGAAGA	AACAGCAGGT	CAATATAGGA	AATTATTCAA	AAATAAAGTT	GAGCATAGTA	780
AATCAGATGA	TCTAGTAACG	GGACTATTAG	AGTGTGGAAC	TCGAAATAGT	TTTGATAAAA	840
CAAGAAGTGC	CTTTCGTTTT	TGTATTTGTG	AGAGAATTCA	GCAACTGAGA	AAAGAAGCTG	900
ATAATGCAAG	AAGAGTAAAA	GATTTTCGATA	CAATGAAAGC	AAAAACTAAA	GAGGCTTTTG	960
AATTGAGTTT	TGTTTTTGAT	AAGGATTTTT	TGAGTGAAAA	TAGAATTCAA	TGGAATGATA	1020
TTTCTCACAA	CAAAAAAGAC	TCTGCAAGTA	AAAGAAAAAC	AATGAAAGAA	GCGGACACAA	1080
TGGATGATAT	TTTTAAGAGG	CTAAAAAATA	ATAAATCTAC	ATATGATCGT	TATGCTGGAT	1140
TCCTTTCTAT	TTGTTTCGATT	ACAGGTTGCA	GACCAGCAGA	AGTTTTAAAG	GGTATAGAGA	1200
TAGTAAGAAA	CAGATATGAG	GATGGTATAT	CTTTTAAAT	ACTTGGTGCA	AAGGTTGGAA	1260
ATGACAGAGG	GCAAAGCGAA	AGAACATTAC	ATTTTGATTT	ATCAAAATAT	CATGATAATG	1320
AGCAAATGAA	TTATATTTTG	TCGCAATTAA	AAGATAATAA	ATTTTTCTAC	AAACCAGATG	1380
GGAAGCTCTA	CAACAGCTTG	AGGCAATACC	TCTACATCCA	ACATAGAACG	TTTTCACTGT	1440
ATACACTTCG	TCACAGGGTT	GCGAGTGATC	TCAAGGCATC	CGGTGCAGAT	GACTTCACCA	1500
TAGCGGCTNT	TTTGGGTCAC	AGAGTGACTC	AAAGCCAGGA	GTTACTACGG	CTATGCTCGT	1560
TCGTGCGNAAG	GTGGTATCGC	TGTAAGTGGT	GTTGAGTGCT	CTGATGTTGT	GAAAGCAAAC	1620
AAGAGTCAGT	TNGCTGTATC	AAGGACTCCG	AGCCAGATCT			1660

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGATCTCAAC	CAGTTTAAAA	TCGCACTTCA	AGAAGTAAAA	ATAGGGGCGG	GCACCGGCTC	60
TTTTTTTGGT	GTTTTTGTAG	TTAGTGGATA	TATCTGTTAG	CTACAGAGAA	AAGCGATTTT	120
AGAGGGTTTG	ACGAGGTTTT	TTGAGCTAT	CCAGGGTTTT	TGGGTTTTTG	GGGTTGGATC	180
AGAAAAGTCG	TTCAAGATTA	TTGACATAAA	GACAGGAAGG	TTTATAACAA	GTACCAGATA	240
CGACAAAACC	AGCTTTGCAG	GCTGGCTTTG	AAGGACTAAA	AGAAGTGGGG	ACTTCTTTGA	300
GTCTTGTAAT	CAAGTTGGTC	AGAAGTTCGAT	TACGATTTGT	AAGTAGAAAT	CTAACTCACA	360
TTTCGCAGAA	AGTCAAACCT	ACCTCTTAGT	TACAACTCAA	AAATTTCCCTA	GCCTTTTCAG	420
ATCCTTAAGC	ATACATATTT	TGTTTTAAACC	GATTGTGTCC	GGTGTTTGGT	GTGGAGCCAT	480
TGATCCGAGT	GGTCAATATG	TGATTGTTCC	CCAAACAGTG	TATGTAGGTC	TAAACGGGGA	540
GTGCTACAAA	AGACCATACC	CGAAACGAGT	GCCTAAGTGT	TTTGGTTATC	AACCAGGTAA	600
GCTATGAGAA	AGCCAGCCA	TAAATGGGGT	TAGGTTGAAG	CAAGTCTTCA	TATGGTGCGA	660
CACAAGGGGT	GTAGTAGGGT	GTCGTCAAAC	TGAAAGGTTT	GATAGCTCTA	AGCTTGTGCT	720
TCTGTGGGTC	AAGCCTCAAG	TGCTGATCTG	TGGTGTCTGC	TACCTGATAA	CTTTCACCTT	780
TTGAGTGA	ATTCAGGAGG	CGAACTATG	GGTCAAGCCC	AGCTTTGCTG	GGGTTCCGCA	840
CATCCAGCTT	ACAGCATTGG	TGCTCTTGCG	AAGCTGAAGC	ACAAAAATCT	AATCCAGGGT	900
TTGGGTTTTT	TATACCAGAA	GCAAAACAAA	AAAATAAAAC	AAAGAAAAAT	TTTCGAGCGA	960
AAAAATATTT	TGGAATTTT	TAAAGGCGAT	ACTTGCTACC	GCACTTTTGC	CATATTTAAA	1020
ACCTGACTAT	CTTTATAAGT	TAATAGATAT	ATCCGTTAGA	TTATAAAGTA	TGTTAAAAAC	1080
GAGTAAAAAC	AATAACTTAT	ATATTTAATT	CTGAATTATA	TTTGACAGTG	ATTATTTAAT	1140
ATATTAAGAG	ATATATCTAT	TAGCTTAAAT	ATAACTAAAA	AAAGAGGTAA	ATATATGGAT	1200
TGTGTATTTA	AAAAAGCATT	AGAAAATGAA	ATAGAACATT	ATAAAAAAGA	CGGTGATATC	1260
AAATCTTTCT	TACAATACTT	GCATTACTTT	GATATAGATA	AAGCATTAAT	TGGTGATGAA	1320
TGTGGCGATA	TTATAAACTC	AAATTTATCC	ATTGATGAAA	GTTTTGATCT	TCTTGATGTT	1380
GAGCACAATT	TCGGCTGGGC	TTTCAATAAA	ATAATACAGA	GACGAAATGA	ATATTTATCA	1440

TCAGCTAAAA	CTGAAAATGA	TTTTAAAAAA	TACTCGTTCT	TTATTCATTC	GATCAATTGG	1500
GAAGAATTTA	ATTACGATGA	GATGAGTACA	ATACATCAAG	AAATGATTAA	AGGATTAGAT	1560
AATTACACAT	ATGGAGAAAT	AACCATATGA	ATAATAAAAT	AAGAGAATAT	ATTGATTTCG	1620
AAATAACAAA	AGATATAAAA	GAAAGTCAGC	TCTTAAAAAT	ATCTGCATTG	ATCGATGTTT	1680
TAAAAGTAGA	TGAAAAATTT	ATTGATGAAG	AGGATTTGCA	ACTAAAGATA	TTGAAAAATAT	1740
CGTATGAAAA	TCCTATTGAT	GATCCAGATG	ATGGCATAAG	AAAATCACAA	TTCGCACGAA	1800
GAAATGCCTA	TGCTTTCCGC	ATTAAAAAAA	CAAGCAAAAA	GAGATCT		1847

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asn	Phe	Leu	His	Trp	Lys	Phe	Glu	Lys	Ile	Arg	Gln	Lys	Lys	Leu	Lys	1	5	10	15
Trp	Lys	Lys	Tyr	Tyr	Tyr	Lys	Lys	Arg	Arg	Ser	Asp	Met	Asp	Phe	Lys	20	25	30	
Ser	Arg	Lys	Leu	Thr	Leu	Asn	Glu	Lys	Lys	Asp	Leu	Glu	Lys	Ile	Tyr	35	40	45	
Ala	Glu	Ser	Glu	Leu	Lys	Ala	Lys	Lys	Leu	Gly	Thr	Gln	Pro	Gly	Val	50	55	60	
Val	Leu	Glu	Met	Thr	Met	Lys	Glu	Met	Met	Lys	Asn	Ile	Asn	Leu	Asp	65	70	75	80
Val	Asn	Glu	Glu	Thr	Ala	Gly	Gln	Tyr	Arg	Lys	Leu	Phe	Lys	Asn	Lys	85	90	95	
Val	Glu	His	Ser	Lys	Ser	Asp	Asp	Leu	Val	Thr	Gly	Leu	Leu	Glu	Cys	100	105	110	
Gly	Thr	Arg	Asn	Ser	Phe	Asp	Lys	Thr	Arg	Ser	Ala	Phe	Arg	Phe	Cys	115	120	125	
Ile	Cys	Glu	Arg	Ile	Gln	Gln	Leu	Arg	Lys	Glu	Ala	Asp	Asn	Ala	Arg	130	135	140	
Arg	Val	Lys	Asp	Phe	Asp	Thr	Met	Lys	Ala	Lys	Thr	Lys	Glu	Ala	Phe	145	150	155	160
Glu	Leu	Ser	Phe	Val	Phe	Asp	Lys	Asp	Phe	Leu	Ser	Glu	Asn	Arg	Ile	165	170	175	
Gln	Trp	Asn	Asp	Ile	Ser	His	Asn	Lys	Lys	Asp	Ser	Ala	Ser	Lys	Arg	180	185	190	
Lys	Thr	Met	Lys	Glu	Ala	Asp	Thr	Met	Asp	Asp	Ile	Phe	Lys	Arg	Leu	195	200	205	

Lys Asn Asn Lys Ser Thr Tyr Asp Arg Tyr Ala Gly Phe Leu Ser Ile  
 210 215 220  
 Cys Ser Ile Thr Gly Cys Arg Pro Ala Glu Val Leu Lys Gly Ile Glu  
 225 230 235 240  
 Ile Val Arg Asn Arg Tyr Glu Asp Gly Ile Ser Phe Lys Ile Leu Gly  
 245 250 255  
 Ala Lys Val Gly Asn Asp Arg Gly Gln Ser Glu Arg Thr Leu His Phe  
 260 265 270  
 Asp Leu Ser Lys Tyr His Asp Asn Glu Gln Met Asn Tyr Ile Leu Ser  
 275 280 285  
 Gln Leu Lys Asp Asn Lys Phe Phe Tyr Lys Pro Asp Gly Lys Leu Tyr  
 290 295 300  
 Asn Ser Leu Arg Gln Tyr Leu Tyr Ile Gln His Arg Thr Phe Ser Leu  
 305 310 315 320  
 Tyr Thr Leu Arg His Arg Val Ala Ser Asp Leu Lys Ala Ser Gly Ala  
 325 330 335  
 Asp Asp Phe Thr Ile Ala Ala Xaa Leu Gly His Arg Val Thr Gln Ser  
 340 345 350  
 Gln Glu Leu Leu Arg Leu Cys Ser Phe Val Xaa Arg Trp Tyr Arg Cys  
 355 360 365  
 Asn Trp Cys  
 370